JOURNAL OF CLINICAL MICROBIOLOGY, Dec. 2011, p. 4412 Vol. 49, No. 12
0095-1137/11/$12.00 doi:10.1128/JCM.05429-11

Letters to the Editor

Cost-Effectiveness of Switch to Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry for Routine Bacterial Identification[▽]

Matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) allows instant identification of microorganisms by analyzing their total protein content (1–3). In September 2009, we switched from conventional biochemical techniques (mainly Vitek 2 and API strips) to MS (Microflex; Bruker Daltonics, Wissembourg, France) for routine identification of all bacterial isolates except for mycobacteria and mycoplasma. Conventional tests were only kept in case of equipment failure or maintenance (10 days per year) and for diagnosis of *Streptococcus pneumoniae*, beta-hemolytic streptococci, and *Shigella* spp., thus entailing a limited stock of identification reagents. After 18 months, we evaluated the benefits in turnaround time and cost in our 3,046-bed acute care university hospital.

Our flow chart was as follows: for each isolate, a portion of 1 to 5 colonies were submitted to MS without protein extraction; if the identification score was not acceptable (<2.0), another round of MS was performed, allowing identification in 97.6% of cases. The accuracy of identification was similar to that reported in the literature (1–4). In our 18-month experience, an average of 3.4 MS tests, each costing \$0.12, were required in order to identify one isolate, i.e., with an identification score of ≥ 2.0, resulting in \$0.41 per bacterial identification at the time of study. When MS identification failed, a relevant housekeeping gene sequence (e.g., *rrs*, *recA*, *sodA*, or *rpoB*) was analyzed (83 isolates a year, compared to 138 in the pre-MS period; $P < 0.05$).

Changes in time to results and workflow were evaluated first. Although the setup times were identical for MS and biochemical techniques, the time to identification was significantly lower with MS, as 93% and 10% of isolates, respectively, were identified within 24 h after inoculation. Early identification allowed us to select appropriate antibiotics to be tested against clinically significant isolates. Subcultures performed in order to achieve a proper inoculum for conventional techniques were drastically cut after MS was implemented, resulting in technical time and culture medium savings. However, time to susceptibility testing results was not reduced, and implementing MS did not allow us to significantly cut down technical staff.

Assessable costs were compared over identical 1-year periods, before and after MS implementation. The overall savings were at least \$177,090. MS identifications of 38,624 isolates between October 2009 and September 2010 cost \$15,836, and conventional identification of 960 remaining isolates over the same period cost \$5,374 (total, \$21,210). The year before, a total of \$193,754 had been spent for 33,320 isolates identified by Vitek 2 cards and API strips (mean unitary cost, \$5.81). In addition, waste disposal decreased from 1,424 kg (cards, pipettes, and suspension media) to 44 kg (MS target cleansing solution and pipette tips), saving \$1,794. Other assessable savings resulted from a \$1,102 cut in subculture medium expenses and a \$1,650 reduction in DNA sequencing. Thus, MS allowed a decrease of 89.3% of the cost of bacterial identifications on the first year.

These data sustain our view to phase out conventional techniques in favor of MS. However, manual handling of microorganisms remains a concern when using MS. Mechanization of the sample preparation would be greatly beneficial, on the way to full laboratory automation.

(A preliminary report of this work was presented at the 111th General Meeting of the American Society for Microbiology, New Orleans, LA, 21 to 24 May 2011.)

The authors declare no conflict of interest.

REFERENCES

1. **Bizzini, A., et al.** 2011. Matrix-assisted laser desorption ionization-time of flight mass spectrometry as an alternative to 16S rRNA gene sequencing for identification of difficult-to-identify bacterial strains. J. Clin. Microbiol. **49:** 693–696.
2. **Cherkaoui, A., et al.** 2010. Comparison of two matrix-assisted laser desorption ionization-time of flight mass spectrometry methods with conventional phenotypic identification for routine identification of bacteria to the species level. J. Clin. Microbiol. **48:**1169–1175.
3. **Demirev, P. A., Y. P. Ho, V. Ryzhov, and C. Fenselau.** 1999. Microorganism identification by mass spectrometry and protein database searches. Anal. Chem. **71:**2732–2738.
4. **Neville, S. A., et al.** 2011. The utility of matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) following introduction for routine laboratory bacterial identification. J. Clin. Microbiol. **49:**2980–2984.

Olivier Gaillot
Nicolas Blondiaux
Caroline Loïez
Frédéric Wallet
Nadine Lemaître
Stéphanie Herwegh
René J. Courcol*
Centre Hospitalier Universitaire de Lille
F-59000 Lille, France

*Centre Hospitalier Universitaire de Lille
Institut de Microbiologie
F-59037 Lille Cedex, France
Phone: +33-320.445.480
Fax: +33-320.444.895
E-mail: rene.courcol@chru-lille.fr

[▽] Published ahead of print on 12 October 2011.